

Fig. 1

Signal peptide
MTRSPALLLLLLGALPSAEAAAR / GPPRMADKVVPRQVARLGRTVRLQCPVEGDPPPLTMWTKDGRTIHSGWS
 1 20 40

IgG1 domain
RFRVLPQGLKVKEVEAEDAGVYVCKATNGFGSLSV***NYTL***IIM / DDISPGKESPGPGGSSGGQEDPASQQWAR
 102

IgG2 domain
 PRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDIMWMKDDQTLTHLEASEHRKKKWTLSLKNLKPEDSG
 161

KYTCRVSNKAGAI***NATY***KVDVIQRTSRKPVLTGTHPV***NTTV***DFGGTTSFQCKVRSDVKPVIQWLKRVEYGS
 224 258

EGRH***NST***IDVGGQKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSFRSAFLTVLPDP
 341

Transmembrane domain
 KPPGPPMASSSSSTSLPWFPVIGIPAGAVFILGTVLLWLCQTKKKKPCAPASTLPVPGHRPPGTSRERSGDK
 374 394

DLPSLAVGICEEHGSAMAPQHILASGSTAG***PKLYPKLYTDV***HTHTHTCTHTLSCGGQGSSTPACPLSVL
 NTANLQALCPEVGIWGPQQVGRIENNGGRVS
 529

Underlined: Signal peptide, IgG1 domain, IgG2 domain, Transmembrane domain

Bold, Italics, underlined: Four putative glycosylation sites

Bold, underlined: putative SHP-2 binding site:

/...../ : Splice sites for FGFR γ

Fig. 2A

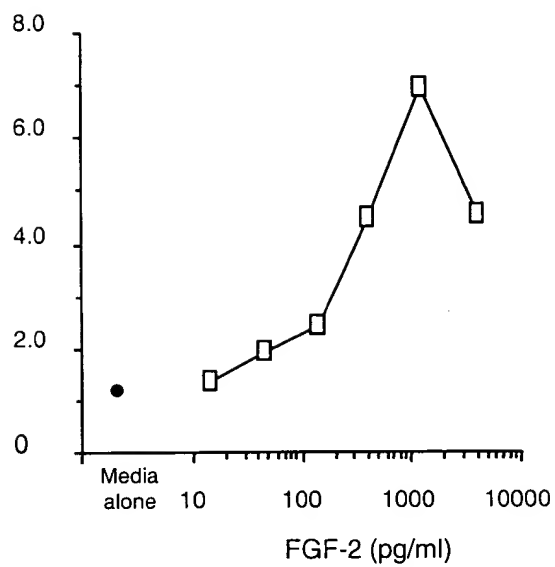


Fig. 2B

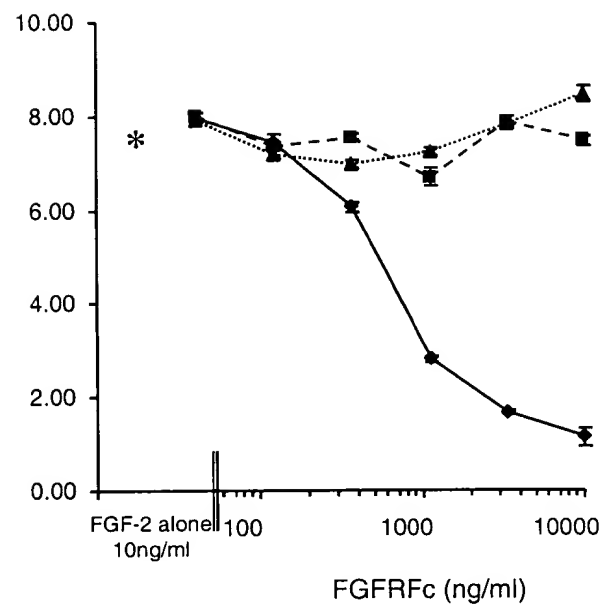


Figure 3 shows the effect of various concentrations of FGFR5 β , FGFR5 γ , FGFR2, and FGF-2 on MTS conversion. The x-axis represents the concentration in nM on a logarithmic scale, and the y-axis represents the MTS conversion (Mean OD \pm SD). The data points are shown with error bars representing standard deviation. The legend indicates that FGFR5 β is represented by open circles, FGFR5 γ by filled triangles, FGFR2 by open squares, FGF-2 by filled circles, and Media by a solid line. The Media control shows a constant MTS conversion of approximately 0.35 across all concentrations. FGFR5 β shows a dose-dependent increase in MTS conversion, starting from approximately 0.35 at 0.0001 nM and reaching approximately 0.8 at 10 nM. FGFR5 γ shows a similar dose-dependent increase, starting from approximately 0.35 at 0.0001 nM and reaching approximately 0.75 at 10 nM. FGFR2 and FGF-2 show no significant effect on MTS conversion, remaining at approximately 0.35 across all concentrations.

Fig. 3

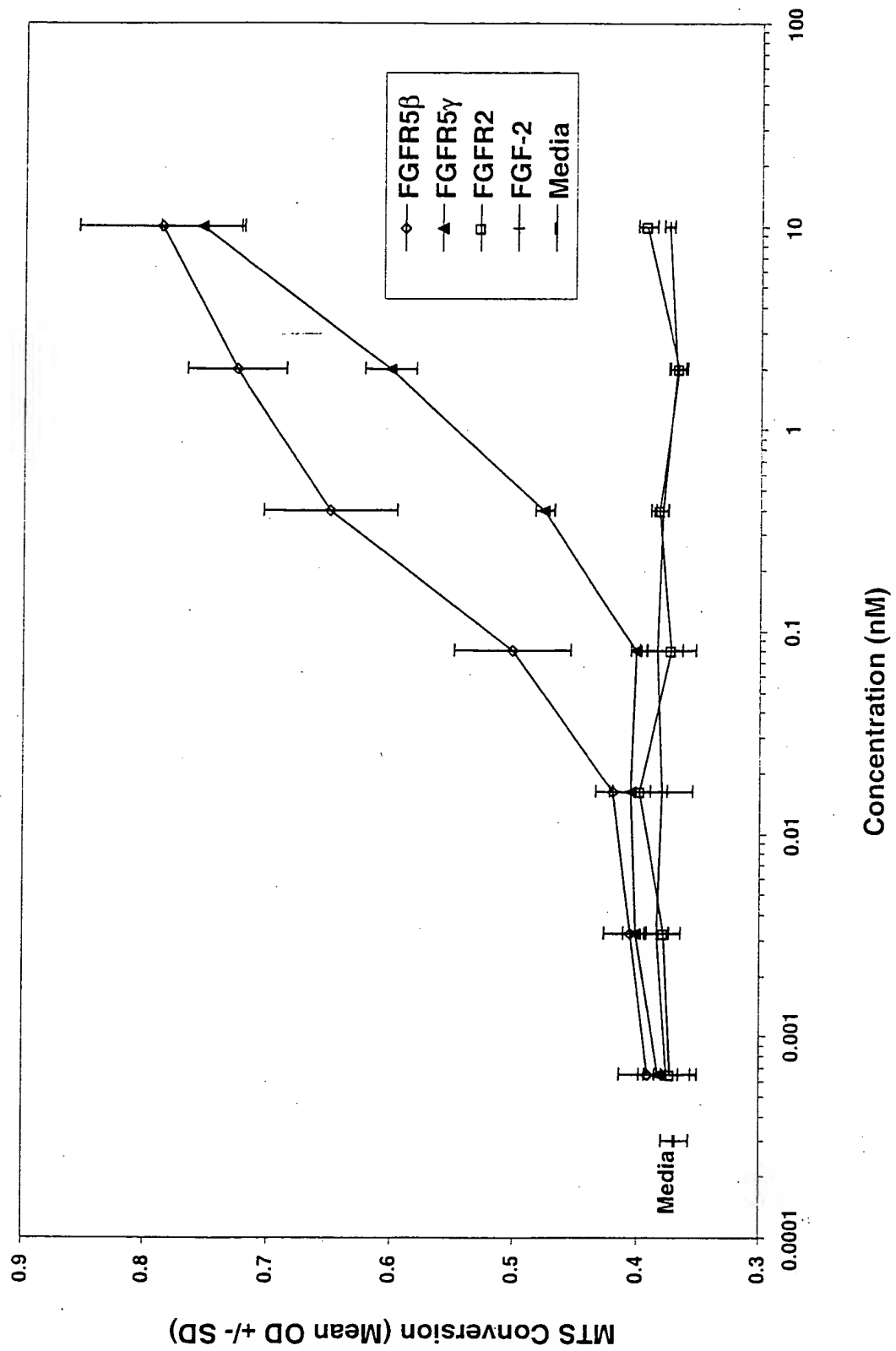


Fig. 4

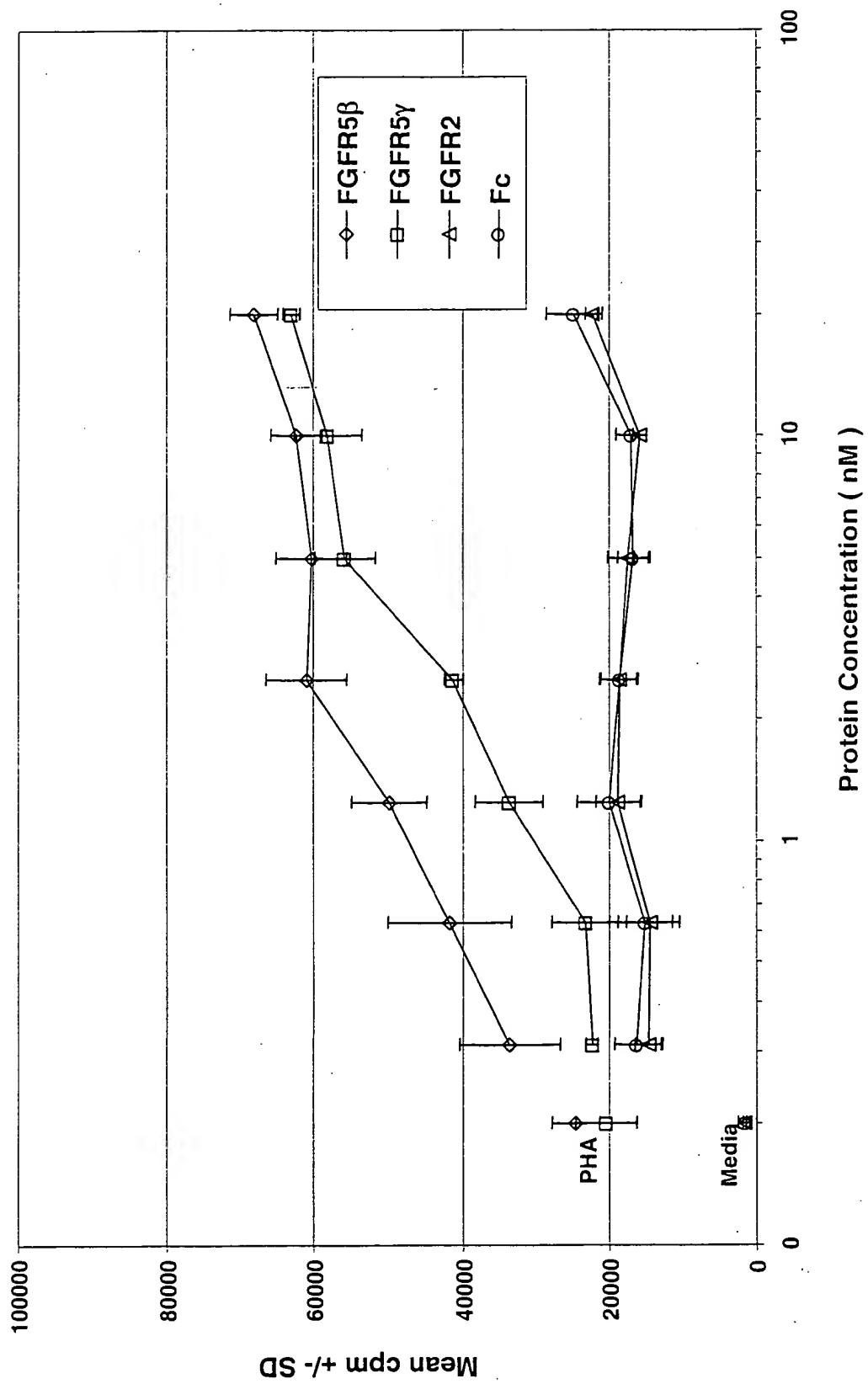


Figure 5 shows the results of the competition assay. The y-axis represents the mean cpm +/- SD, and the x-axis represents the protein concentration in nM. The legend indicates four conditions: FGFR5β (open circles), FGFR5γ (open squares), FGFR2 (open triangles), and Fc (open circles). The data shows that FGFR5β and FGFR5γ have higher binding affinity than FGFR2 and Fc, with FGFR5β showing the highest binding across the concentration range.

Fig. 5

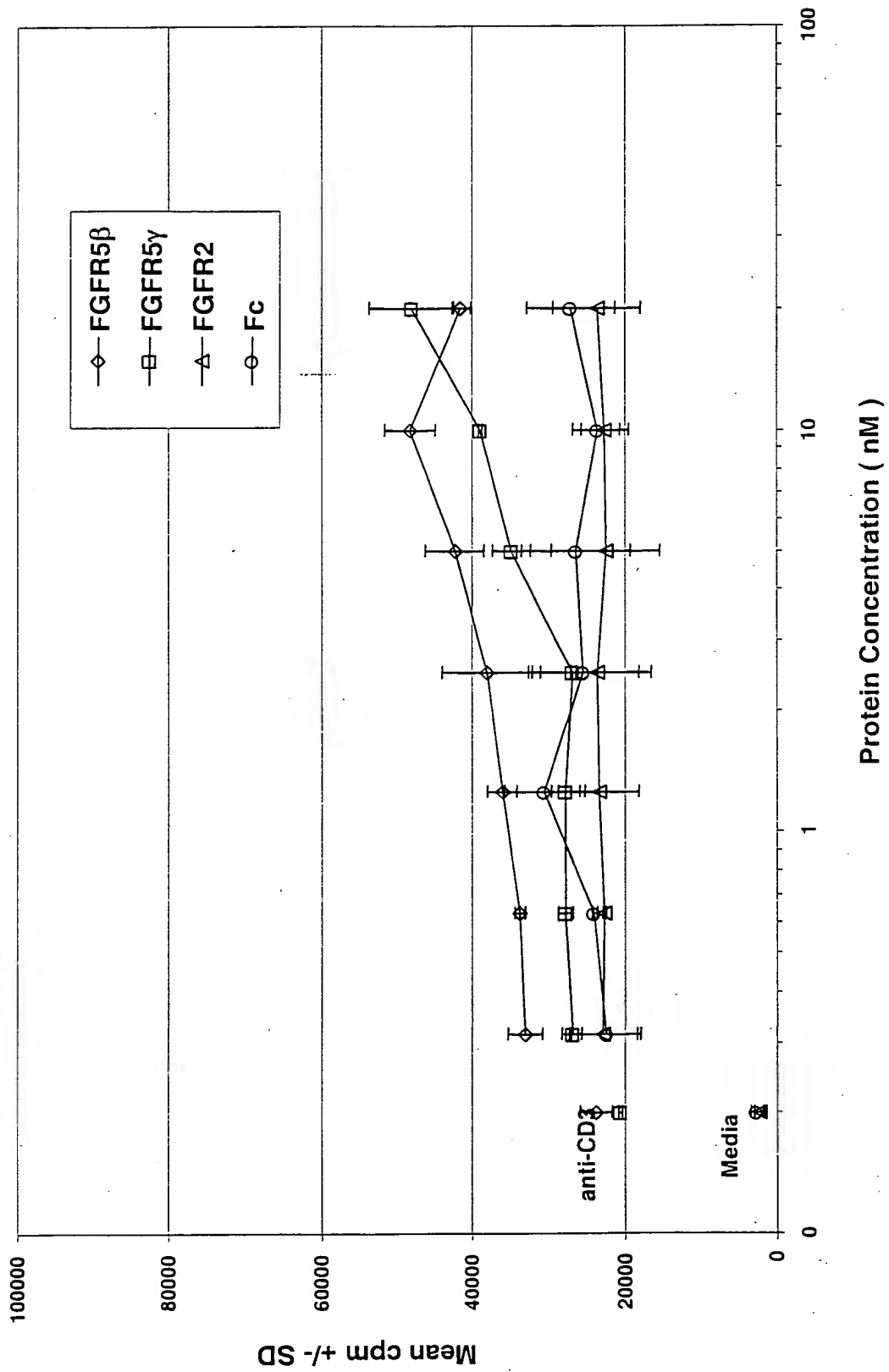


Fig. 6

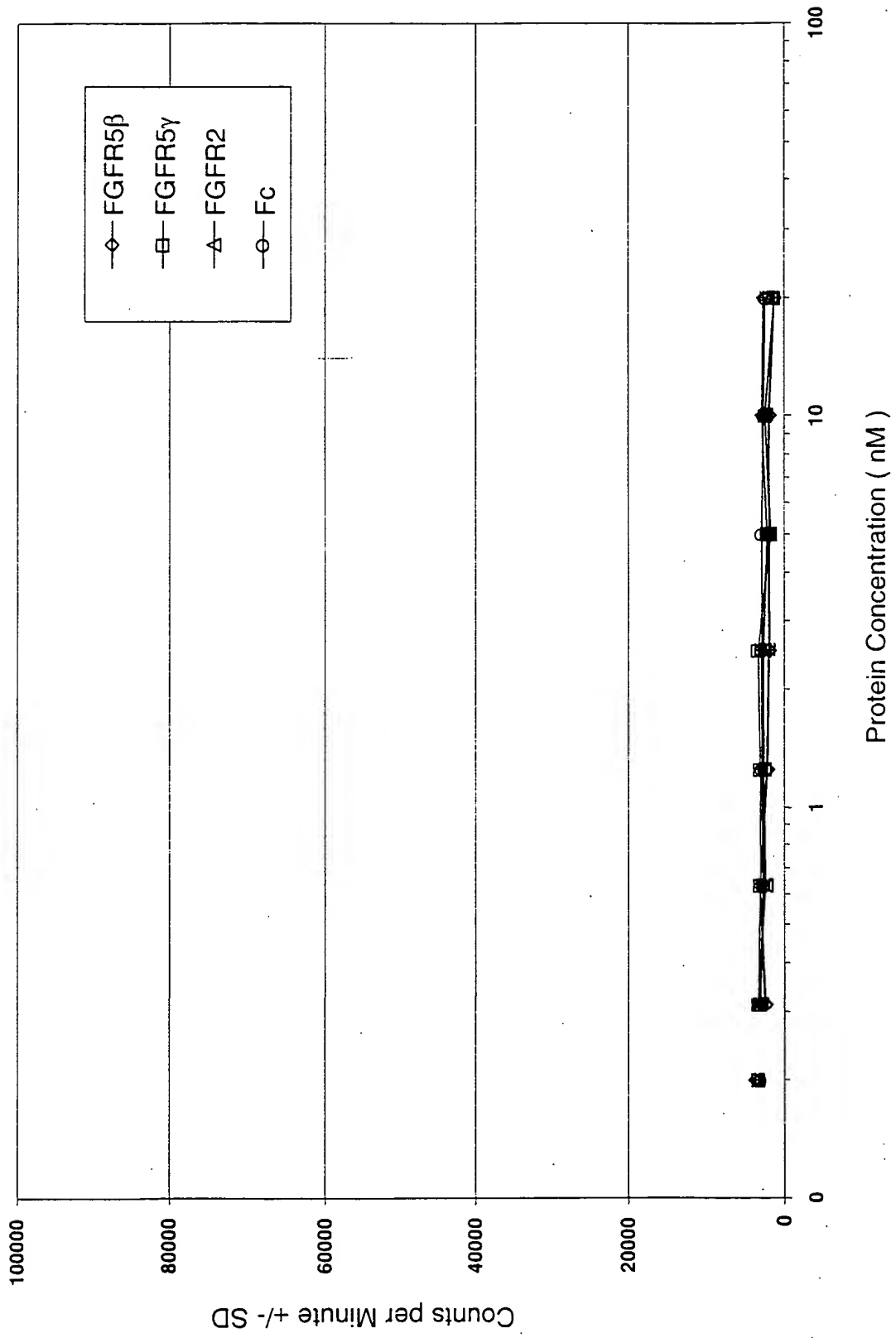


Fig. 7

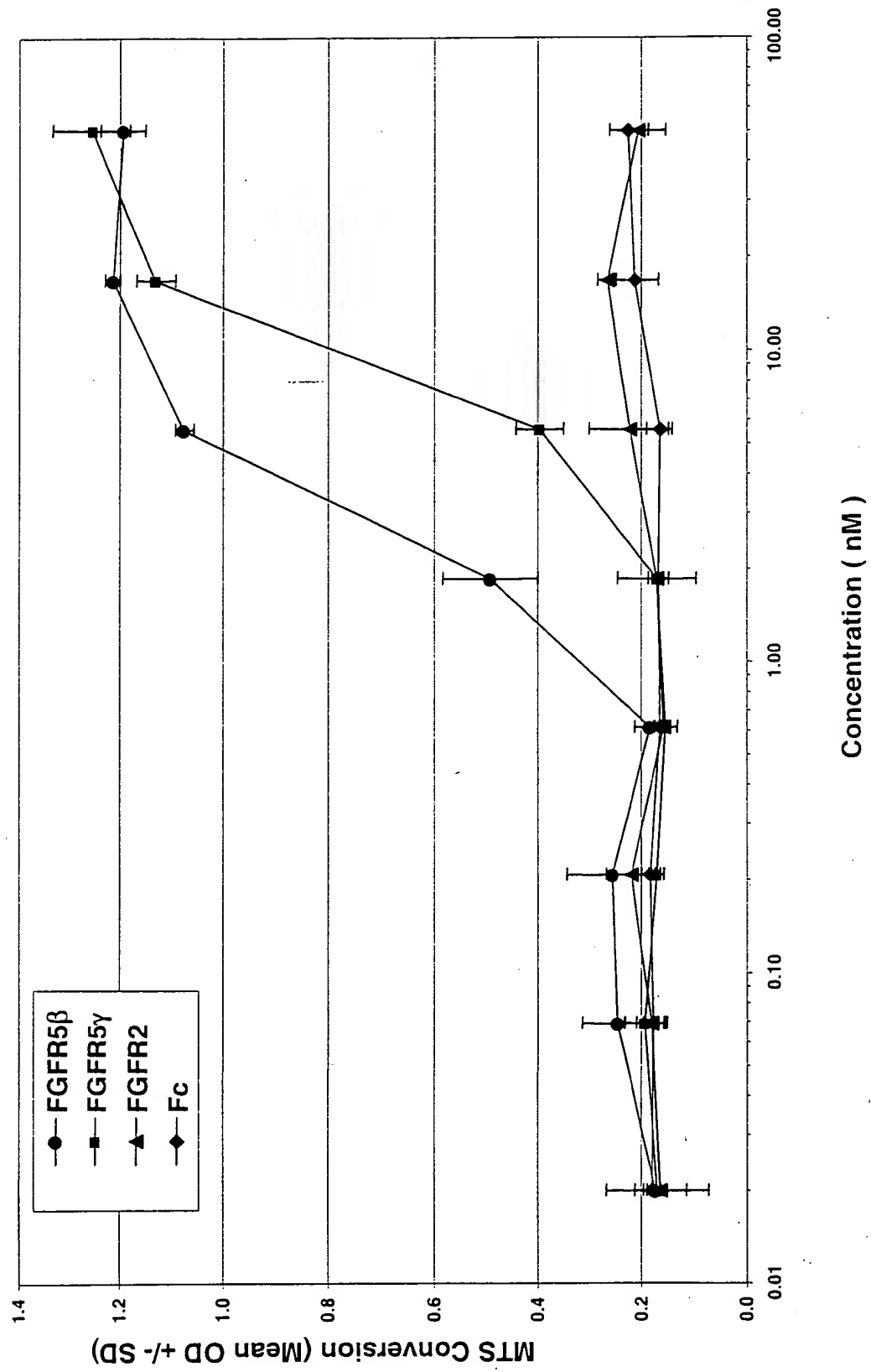


Fig. 8

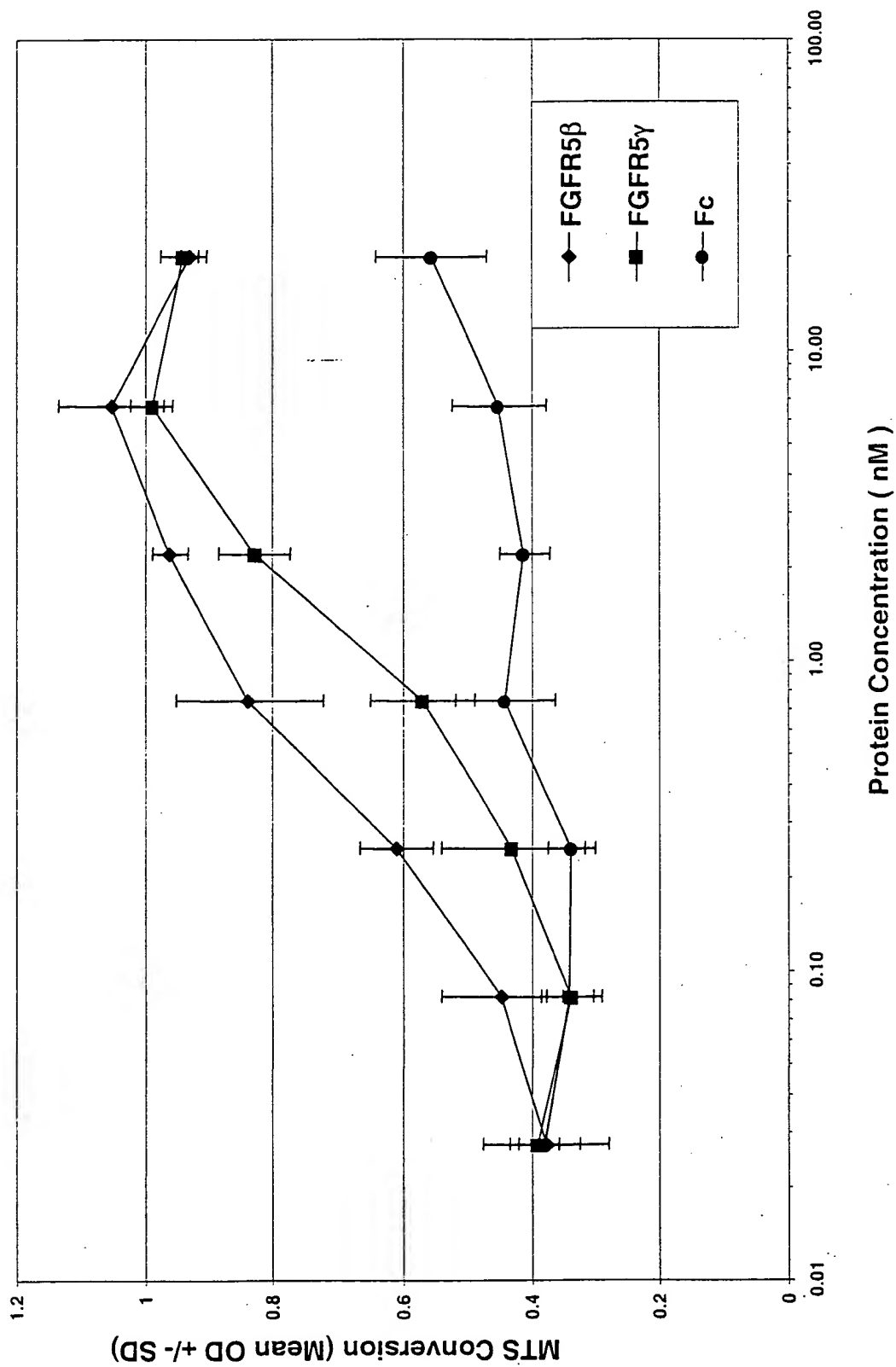
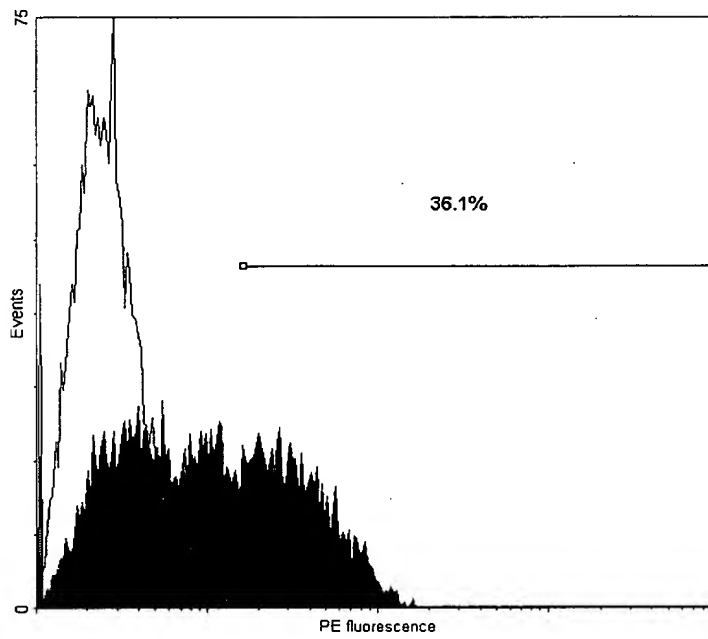


Fig. 9

FGFR5 β -treated PBMC

Overlay Plot 1



FGFR5 γ -treated PBMC

Overlay Plot 2

